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P0372 Molecular epidemiology of clinical Clostridium difficile isolates obtained from clinics and hospitals in the Pretoria region, South Africa

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Background: *Clostridium difficile* is the leading cause of health-care associated diarrhoea globally. The molecular epidemiology of *C. difficile* in the Pretoria region in South Africa is unknown. The aim of this study was to determine the genetic relatedness of clinical *C. difficile* isolates in Pretoria.

Materials/methods: A total of 97 stool specimens submitted to the Diagnostic Division of the Department of Medical Microbiology/National Health Laboratory Service were collected from June 2016 to April 2017 after routine diagnosis. Patient clinical data was collected by analysis of patient records and consulting the attending physician. Stool specimens were collected that tested positive for toxin A/B by the C Diff Quik Chek Complete® assay or positive for the *tcd*B gene by the Cepheid GeneXpert *C. difficile*® real-time PCR assay according to a two-step algorithm. Stool specimens were treated with the alcohol shock method and cultured anaerobically on cycloserine-cefoxitin fructose agar at 37°C for 48 to 72 h. Genomic DNA extraction was performed using a commercial kit. The toxin genes were detected using a multiplex-PCR assay. Molecular typing was performed using PCR ribotyping.

Results: The patient demographics were as follows: 64% (62/97) female and 36% (35/97) male with a mean age of 40 years. The co-morbid conditions were diverse, however 31% (30/97) of patients were HIV positive and 15% (15/97) of patients were diagnosed with tuberculosis. The most commonly used antibiotics were piperacillin-tazobactam (20%) followed by amoxicillin (12.37%). Toxin A (*tcd*A) and toxin B (*tcd*B) were detected in all isolates, however, the binary toxin was not detected. The PCR ribotyping showed a high clonality among the isolates obtained from patients presenting with *C. difficile* infection.

Conclusions: The high prevalence of HIV and tuberculosis among the patients contributes significantly to increased hospitalisation and exposure to antimicrobials which increases the risk for acquiring CDI. The PCR ribotyping data showed a high clonality among the *C. difficile* isolates circulating in clinical settings in the Pretoria region. Surveillance of hypervirulent pathogenic strains of *C. difficile* such as 027 and 078 are important to prevent outbreaks of CDI.